

SEQUENCE LISTING

I. GENERAL INFORMATION:

II. APPLICANT: Thomas, Lawrence J.

III. TITLE OF INVENTION: PLASMID BASED VACCINE FOR TREATING ATHEROSCLEROSIS

IV. NUMBER OF SEQUENCES: 10

V. CORRESPONDENCE ADDRESS:

A. ADDRESSEE: Tarkwich & Associates
 B. STREET: 130 Bishop Allen Drive
 C. CITY: Cambridge
 D. STATE: Massachusetts
 E. COUNTRY: USA
 F. ZIP: 02119

VI. COMPUTER READABLE FORM:

A. MEDIUM TYPE: Floppy disk
 B. COMPUTER: IBM PC compatible
 C. OPERATING SYSTEM: Windows 95/98
 D. SOFTWARE: Word 97

VII. CURRENT APPLICATION DATA:

A. APPLICATION NUMBER: (not yet assigned)
 B. FILING DATE: 30 April 2001
 C. CLASSIFICATION:

VIII. PRIOR APPLICATION DATA:

A. APPLICATION: 08/640,713
 B. FILING DATE: 01 May 1995 (01.05.96)

IX. PRIOR APPLICATION DATA:

A. APPLICATION: 08/800,967
 B. FILING DATE: 21 February 1997 (01.02.97)

X. PRIOR APPLICATION DATA:

A. APPLICATION: 09/171,969
 B. FILING DATE: 29 October 1998 (29.10.98)

XI. ATTORNEY/AGENT INFORMATION:

A. NAME: Leon R. Tarkwich
 B. REGISTRATION NUMBER: 30,237
 C. REFERENCE DOCKET NUMBER: TCS 414.2 US-1

II. INFORMATION FOR SEQ ID NO: 1:

A. SEQUENCE CHARACTERISTICS:

1. LENGTH: 1488 base pairs
 2. TYPE: nucleic acid
 3. STRANDEDNESS: single

4. TOPOLOGY: linear

5. MOLECULE TYPE: cDNA

6. HYPOTHETICAL:

7. ANTI-SENSE:

8. FEATURE: Structural coding sequence (1)

Human Rabbit cETP

A NAME:

B LOCATION:

X PUBLICATION INFORMATION:

A AUTHORS: Nagashima, Mariko, et al.

B TITLE: Cloning and mRNA tissue

distribution of rabbit

cholesteryl ester transfer

protein

C JOURNAL: J. Lipid Res.

D VOLUME: 29

E ISSUE:

F PAGES: 1643 1649

G DATE: 1988

H RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 1488

X1 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCTCCCAAG GCGCCTCTA CGAGGCTGGC ATCTGTGTG GCATCACCAA	50
GGCGCCCTC TTGGTGTGA ACCAAGAGAC GGCCTAAGGTG GTCCACACCG	100
CCTTCCAGCG CGCGGGCTAT CCGGACGTCA GCGGCGAGAG GCGCGTGATG	150
CTCTCGGGC GGGTCAAGTA CCGGTGTGAC AACTTCCAGA TCAGGCGAGT	200
GTCCATCGCG AGCAGCGAGG TGGAGCTGGT GGAAGCCAAAG ACCATCGAGC	250
TGCGCATCCA GAAGTGTGTC GTGGTCTTCA AGGCGAGGCTT GAATACAGC	300
TACACGAGTG CCGGGGGCTT GGGCATCAAT CAGTGTGTG ACTTGGAGAT	350
AGATGTGCG ATTGAGCTG AGATCAACAG AGAGGTGAGC TGGAGGTTG	400
GCAGTGTGCG CAGCAATGCG CCGGAGTCTT ACCGTGGCTT CCATAAAGTG	450
GTCTGCAAG TCGAGGGCGA GGGGAGCGG GGTGTGTGCA AGCAGGTCTT	500
CACAAACTTG ATCTGTGTC GGTGAAAGT GATGTGAAAG CAGAGGTGT	550
GCAATCAGAT CAACAGCAGC TCGAAGATCA TGGTGTGCTT TGTGAGAGC	600
AGGGCGCGCA GCACTGTGTC AGATGAGAGC ATCGGGGTGG ACATTTGCTT	650
CAGGGGGCGC CCTGTGATCA CAGCCACCTA CGGTGAGTGC CATCACAAGC	700
ATTACTTCAG GCATAGAGAG GTCTCGGAGG CATTCCGCTT CCGCGGCTTC	750
AGGGGGGTTC TTCTGGGGA GTCCCGCATG CTGTACTTCT GGTGTGCGA	800
TAAATGTTC AACCTCTGCG CAGGGGGCGC CTTCAGGAG GCGGTGTG	850
TATTAAGCT CAGAGGGAT GATTCAGAG AAGTGTGGA GAGGAGGCT	900
TAAAGAGG AGCAGGAAT GTTCAGGAG GTTCAGAGG GTTTTGGAG	950
CAAGAGAG CAGTGTGTC TAAATGTTC AAGTGTTC	1000

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GCCAGAACCC GGGTGTGGTG GTGTGTGTTT CCGTCCGCGT GACGTTCCGC 1050
TTCCCCCGCC CASATGGCCG AGAAGCTGTG GCCTACAGGT TTGAGGAGGA 1100
TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAAG CTCTTCCTAC 1150
ACCTCTTGGG TTTCCAGTGG GTGCCCCGCC GCGGAAAGGC AGGCAGCTCA 1200
GCCAAATCTCT CCGTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCCAACCT 1250
GACTGAGAGC CGCTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG 1300
TCACGGTGGG CATCCCGGAG GTCATGTCTC GGTCCGAGGT GCGCTTCACA 1350
GCGCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA 1400
GATTATCACT CTCGATGGCT GCTGTGTGCT GCAGATGGAC TTGGGTTTTG 1450
CCAAGCACCT GCTGGTGGAT TTCTGCAGA GCTGAGG 1486

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2. INFORMATION FOR SEQ ID NO:2:

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1. SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 496 amino acids
   (B) TYPE: amino acid
2. TOPOLOGY: linear
3. MOLECULE TYPE: protein
4. HYPOTHETICAL:
5. ANTI SENSE:
6. FEATURE:
   A NAME: Amino acid sequence for mature
rabbit CETP protein.
   B LOCATION:

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8. PUBLICATION INFORMATION:
   A AUTHORS: Nagashima, Mariko, et al.
   B TITLE: Cloning and mRNA tissue
distribution of rabbit
cholesteryl ester transfer
protein
   C JOURNAL: J. Lipid Res.
   D VOLUME: 29
   E ISSUE:
   F PAGES: 1643 - 1649
   G DATE: 1988
   H RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 496

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9. SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Phe Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
1          5          10
Met Ile Thr Lys Phe Ala Leu Leu Val Leu Asn Glu Glu
11         15         20         25

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Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
30 35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu
40 45 50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
70 75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
95 100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
120 125 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
135 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Ala Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170 175 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
210 215 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
225 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235 240 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu

168

270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
275 280 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln
290 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
300 305 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
315 320 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
330 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
340 345 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe
355 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser
365 370 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys
380 385 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu
395 400

Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
405 410 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu
420 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met
430 435 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser
445 450 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile
460 465

Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe
470 475 480

Lys Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser
485 490

Leu Ser
495

2 INFORMATION FOR SEQ ID NO: 3:
 1 SEQUENCE CHARACTERISTICS:
 A LENGTH: 1428 base pairs
 B TYPE: nucleic acid
 C STRANDEDNESS: single
 D TOPOLOGY: linear
 E MOLECULE TYPE: cDNA
 F HYPOTHETICAL
 G ANTI-SENSE:
 H FEATURE
 A NAME: Structural coding sequence for
 mature human CETP
 B LOCATION:
 I PUBLICATION INFORMATION:
 A AUTHORS: Drayna, Dennis, et al.
 B TITLE: Cloning and sequencing of
 human cholesteryl ester
 transfer cDNA
 C JOURNAL: Nature
 D VOLUME: 327
 E ISSUE:
 F PAGES: 632 - 634
 G DATE: 18-JUN-1987
 H RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

31 SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCCTCCAAAG GCACCTGCGA CGAGGCAGGC ATCGTGTCGC GCATCACCAG	50
TCCTGCCCTC CTGGTGTGGA ACCACGAGAC TCCCAAGGTC ATCCAGACCG	100
CTTCCAGCG AGCCAGGTAG CGAGATATCA CCGGCGAGAA GGGCATGATC	150
CTCTTGCGCC AAGTCAAGTA TGGGTTGCAG AACATCCAGA TCAGCCACTT	200
CTCCATCGCC ACCAGCCAGC TGGAGCTGGT GGAAGCGAAG TCCATTGATC	250
TCTGCATTCA GAACCTGCTT CTGGTCTTCA AGGGGACCGT GAAGTATGCG	300
TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT	350
TCAGTCTGCC ATTGACCTGC AGATCAAGAC ACAGCTGACC TGTCACTCTG	400
GTAGAGTGGG GAGCGATGCG CCGACTGCT ACCTGTCTTT CCGTAAGCTG	450
AGGTGAGTTC TCCAGCGGGA GCGAGACCGT GGGTGGATCA AGCAGTCTT	500
TAGAAATTTG ATCTCCTTCA CCGTGAAGCT GGTCTGTAAG GACAGATCT	550
ATAAAGAGAT GAAGCTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA	600
AGAGTGTGTA GCATGCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT	650
TAGATTTGAT AGGTGATTA CAGCTTCTA CCGGGAGTCC CATCAGAAAG	700
CTGATTTTAT TTATAGAAAT GTCTGAGAGG AGCTGCTCTT GGTGATTTT	750

123TCACAC TCCGGGGGA GTCCCGCATG CTGTACTTCT GGTTCCTCA	800
GGGATCTTC CACTCGGTGG CCAAGGTAGG TTTCAGGAT GGCCCGCTCA	850
TGTTGAGCTT GATGGGAGAG GATTTCAAGG CACTGCTGGA GACCTGGGGC	900
TTCAACACCA ACCAGGAAAT CTTCGAAGAG GTTGTGGGGC GCTTGGGCA	950
CCAGGGCCAA GTACCGGTGC ACTGGGTCAA GATGGGCAAG ATGTGGTGGC	1000
AAAACAGGG AGTGGTGGT AATTCTTCAG TGATGGTGAA ATTCTCTTT	1050
CCAGCGCCAG ACCAGCAACA TTCTGTAGCT TACAGATTG AAGAGGATAT	1100
CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC	1150
TCITGGATTT CCAGATTACA CCAAGAGCTG TTCCAACTT GACTGAGAGC	1200
AGCTCCGAGT CCATCCAGAG CTTCCTGGAG TCAATGATCA CCGCTGTGGC	1250
CATCCCTCAG GTCATGTCTC GGTTCGAGGT AGTGTTTACA GCGCTCATGA	1300
ACAGCAAAGG CGTGAGGCTC TTGGACATCA TCAAGCTGA GATTATCACT	1350
CCAGATGGCT TCCTGTGTGT GCAGATGGAC TTTGGCTTCC CTGAGCACT	1400
GGTGTGGAT TTCTCCAGA GCTTGAGC	1428

1 INFORMATION FOR SEQ ID NO: 4:

1 SEQUENCE CHARACTERISTICS:

A LENGTH: 476 amino acids

B TYPE: amino acid

D TOPOLOGY: linear

I MOLECULE TYPE: peptide

III HYPOTHETICAL:

IV ANTI SENSE:

IX FEATURE:

(A) NAME: Amino acid sequence of mature human

DETP

B LOCATION:

X PUBLICATION INFORMATION:

A AUTHORS: Drayna, Dennis, et al.

B TITLE: Cloning and sequencing of human acyl-coenzyme A:cholesterol acyltransferase cDNA

C JOURNAL: Nature

D VOLUME: 327

E ISSUE:

F PAGES: 632-634

G DATE: 18 JUN 1987

H RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO 476

XI SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1 5 10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
15 20 25

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser
30 35

Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40 45 50

Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
55 60 65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
70 75

Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
80 85 90

Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
95 100

Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105 110 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
120 125 130

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
135 140

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
145 150 155

Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
160 165

Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170 175 180

Ile Lys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
185 190 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
210 215 220

Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
225 230

Ile Phe Ile Tyr Lys Asn Val Ser Gln Asp Leu Phe Leu
235 240 245

Pro Tyr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
250 255 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
265 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
275 280 285

Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
290 295

Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
300 305 310

Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
315 320 325

Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
330 335

Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
340 345 350

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
355 360

Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
365 370 375

Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
380 385 390

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
395 400

Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
405 410 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
420 425

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
427 435 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
445 450 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
460 465

Val Asp Phe Leu Gln Ser Leu Ser
470 475

1 SEQUENCE CHARACTERISTICS:
 A LENGTH: 169 base pairs
 B TYPE: nucleic acid
 C STRANDEDNESS: single
 D TOPOLOGY: linear
 E1 MOLECULE TYPE:
 E1.1 HYPOTHETICAL:
 E1.2 ANTI SENSE:
 E1.3 FEATURE:
 A NAME:
 B LOCATION:

x1 SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

CCGCCCCCGCA TGCAGTACAT CAAGGGCAAC TCCAAGTTCA TCGGCATCAC      50
GGAGCGGCTC CCGCGCCAG ATGGCGGAGA AGGTGTGGCC TACAGGTTTG      100
AGGAGGATAT CTTCGGTTTT CCCAAGCACC TGCTGGTGGG TTTCCTGCAG      150
AGCTGAGCT AGCGGGCGC                                     169

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2 INFORMATION FOR SEQ ID NO: 6:
 1- SEQUENCE CHARACTERISTICS:

A LENGTH: 169 base pairs
 B TYPE: nucleic acid
 C STRANDEDNESS: single
 D TOPOLOGY: linear
 E1 MOLECULE TYPE: DNA
 E1.1 HYPOTHETICAL:
 E1.2 ANTI SENSE:
 E1.3 FEATURE:
 A NAME: Complementary strand to SEQ ID NO:5
 B LOCATION: 1 to 169

x1 SEQUENCE DESCRIPTION: SEQ ID NO:6:

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CCCCCCCCCTA GTTAGGCTC TGCAGGAAAT CCACAGGCAG CTGCCTG333A      50
AAACCGAAGA TATCTCTCTC AAACCTGTAG GGCACAGCTT CTGGGCCATC      100
TGGCGGGGGG AAGGCTTCCG TGATCCCGAT GAAGTTGGAG TTGCGCTTGA      150
TGTACTGGAT GCGGGCGCG                                     169

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3 INFORMATION FOR SEQ ID NO:7:

1 SEQUENCE CHARACTERISTICS:
 A LENGTH: 50 amino acids
 B TYPE: amino acid
 C TOPOLOGY: linear
 E1 MOLECULE TYPE: peptide
 E1.1 HYPOTHETICAL:
 E1.2 ANTI SENSE:
 E1.3 FEATURE: amino acid sequence of peptide encoded
 by bases 11 to 169 of SEQ ID NO:5

A NAME:
B LOCATION:

XI. SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1 5 10

Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
15 20 25

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
30 35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
40 45 50

II. INFORMATION FOR SEQ ID NO:8:

1. SEQUENCE CHARACTERISTICS:

A LENGTH: 1608 base pairs

B TYPE nucleic acid

C STRANDEDNESS: Single

D TOPOLOGY: linear

E MOLECULE TYPE:

F HYPOTHETICAL:

G ANTI SENSE:

H FEATURE:

A NAME translational stop codon

B LOCATION: 1606 1608

XI. SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGCGTCATG ATGTTGTGGA TTCTTCTAAA TCTTTTGTGA TGGAAAACTT 50
TTTTCGTAC CACGGACTA AACCTGTTA TGTAGATTCC ATTCAAAAAG 100
GTATACAAAA GCCAAAATCT GTTACACAAG GAAATTATGA CCATGATTGG 150
AAAGGGTTTT ATAGTACCGA CAATAAATAC CACGCTCGGG GATACTCTGT 200
AGATAATGAA AACCCCTCT CTGAAAAAGC TGGAGCCCTG GTCAAACTGA 250
GTATGCGAG ACTGACGAAG GTTCTGGCAG TAAAGTGA TAATGCCGAA 300
AGATTAAAG AAGATTAGG TTAAAGTCT ACTGAAGCTT TATGCGAG 350
ATTGCGAAG GAAGAGTTA TCAAAAGCTT CGGTGATGCT CTTTCCTCT 400
TATGCTCAG CTTTCCTTC CCGAGGGGGA GTTCTAGCGT TCAATATATT 450
TATGCTCAG AACAGCGGAA AGGTTAAGC GTAGAACTTG AGATTATTT 500
TATGCTCAG AAAAAGCTG GCGAAATGC CATCTATGAG TATATGCTT 550
TATGCTCAG AAAAATCT TTAGGCGAT CATTAGTAT GTATTCTTA 600

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133ATATAATC TTGATTGGGA TGTCATAAGG GATAAAACTA AGACAAAGAT 650
AGAGTGTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC 700
CCATATAAAC AGTATCTGAG GAAAAAGCTA AACAATACCT AGAAGAATTG 750
CATCAAAACGG CATTAGAGCA TCCGGAATTG TCAGAACTTA AAAACCTTAT 800
TGGGACCAAT CCTGTATTTCG CTGGGGCTAA CTATGCCGCG TGGGCATTA 850
ACCTTGGGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900
ACTGCTGCTC TTTCGATACT TCCGTGATAT CGTAGGCTAA TGGGCATTGC 950
AGACGCTGCC GTTCACGACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000
GTTTATCGTC TTTAATGGTT GGTCAAGCTA TCCATTGGT AGGAGAGCTA 1050
GTTCATATTG GTTTCGGTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100
ATTTCAGCTA GTTCATAATT GGTATAATCG TCCGCGCTAT TCTCCGCGCG 1150
ATAAAACGCA ACCATTTCTT CATGAGGGGT ATGCTGTCAG TTGGAACAGT 1200
GTTGAAGATT CGATAATCCG AACCGTTTTT CAAGGGGAGA GTGCGCACGA 1250
CATAAAAATT ACTGCTGAAA ATATCTGGGT TCGAATGCGG GGTGTCTTAC 1300
TAGCGACTAT TCCGTGAAAG CTGCACTTA ATAACTGAA GACTCATATT 1350
TGGTAAATG GTCGGAAAAA AAGGATGCTT TCGAGAGCTA TAGACGGTGA 1400
TCTAACTTTT TGTGCGCTTA AATCTCTGT TTATGTTGTT AATGTTGTGC 1450
ATCGCATCTT TCACGTGCA TTTCAAGAA GCAGCTCGGA GAAAAATCAT 1500
TCTAATGAAA TTTCGTGCGA TTCCATAGGC GTTCTTGGGT ACCAGAAAAC 1550
AGTAAATCAC ACCAAGGTTA ATTCTAAGCT ATCGGTATTT TTGAAATCA 1600
AAAGCTGA 1608

```

2 INFORMATION FOR SEQ ID NO:9:

1 SEQUENCE CHARACTERISTICS:

A LENGTH: 535 amino acids

B TYPE: amino acid

C TOPOLOGY: linear

11 MOLECULE TYPE: protein

111 HYPOTHETICAL:

12 ANTI-SENSE:

13 FEATURE: A NAME:
B LOCATION:

14 SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1 5 10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
15 20 25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr
30 35 40

Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr
45 50 55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
60 65 70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
75 80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn
85 90 95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
100 105 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
115 120 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
130 135 140

Ala Gln Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
145 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu
155 160 165

Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met
170 175 180

Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
185 190 195

Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
200 205 210

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
215 220

Phe Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
225 230 235

Phe Ala Gln Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
240 245 250

Ile Ala Leu Gln His Phe Glu Leu Ser Glu Leu Lys Thr Val
255 260 265

Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala
270 275 280

Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala
285 290

Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro
295 300 305

Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
310 315 320

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
325 330 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
340 345 350

Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
355 360

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro
365 370 375

Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp
380 385 390

Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile
395 400 405

Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile
410 415 420

Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu
425 430

Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
435 440 445

His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
450 455 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
465 470 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
480 485 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
495 500

Phe Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
505 510 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Gln
520 525 530

100 100 100
535

1. INFORMATION FOR SEQ ID NO:10

1. SEQUENCE CHARACTERISTICS:

A LENGTH: 21 amino acids

B TYPE: amino acid

C TOPOLOGY: linear

D MOLECULE TYPE: protein

E HYDROPHILIC:

F ANTI-SENSE:

G FEATURE:

A NAME:

B LOCATION:

2. SEQUENCE DESCRIPTION: SEQ ID NO: 10:

100 Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
1 5 10

105 Lys Val Ser Ala Ser His Leu Glu
15 20